In order to maintain the binding interaction during the electrophoretic process, non-denaturing gel matrix materials and conditions in the absence of reducing agent are typically preferred. Appropriate conditions to the particular assay and components thereof will be well known to one skilled in the art.

REMARKS

Attached hereto is a marked-up version of the changes made to the specification by current amendments. The attached page captioned "Version With Markings to Show Changes Made." No new matter has been added.

In response to the Notice to Comply with Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures, Applicants respectfully submit herewith a Sequence Listing which contains SEQ ID NO:1, a sequence set forth in the instant specification. Applicants have not enclosed a Sequence Listing corresponding to the markers identified in Table 1. Applicants respectfully submit that Table 1, which sets forth all of the markers of the present invention, contains GenBank GI numbers for each marker, which are incorporated by reference. As set forth in the specification on page 94, lines 21-26:

> The description for the fields of Table 1 is listed below.
> 'GI #' refers to the NCBI accession number assigned respectively to the protein encoded by the marker gene and the cDNA corresponding to the protein. The amino acid sequence of each protein and the nucleotide sequence of the corresponding cDNA are disclosed in NCBI databases (see, for example http://www.ncbi.nlm.nih.gov/Entrez/nucleotide.html). All NCBI database sequences referenced by the listed GI numbers are expressly incorporated herein by reference.

Applicants further submit that the sequence content corresponding to a GenBank GI identification number is fixed and cannot be altered by addition or correction. Therefore, Applicants have not enclosed a Sequence Listing in Response to the Notice to Comply with Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures for the markers identified in Table 1.

CONCLUSION

The Commissioner is hereby authorized to charge payment of any fees under 37 C.F.R. 1.16 and 1.17 during the pendency of this application or credit any overpayment to Deposit Account No. 12-0080.

Respectfully submitted,

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Dated: **September 25, 2002**

VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the Specification:

Please insert after the last page of the specification, before the claims, the Sequence Listing submitted herewith, which contains SEQ ID NO:1.

Replace the paragraph at page 30, line 25 through page 31, line 3 of the specification with the following paragraph,

RNA from a source to express the cDNA corresponding to a given tag is first converted to double-stranded cDNA using any standard cDNA protocol. Similar conditions used to generate cDNA for SAGE library construction can be employed except that a modified oligo-dT primer is used to derive the first strand synthesis. For example, the oligonucleotide of composition 5'-B-TCC GGC GCG CCG TTT TCC CAG TCA CGA(30)-3'**(SEQ ID NO:1)**, contains a poly-T stretch at the 3' end for hybridization and priming from poly-A tails, an M13 priming site for use in subsequent PCR steps, a 5' Biotin label (B) for capture to strepavidin-coated magnetic beads, and an AscI restriction endonuclease site for releasing the cDNA from the strepavidin-coated magnetic beads. Theoretically, any sufficiently-sized DNA region capable of hybridizing to a PCR primer can be used as well as any other 8 base pair recognizing endonuclease.

Replace the paragraph at page 83, lines 1-28 of the specification with the following paragraph,

Alternatively, in another embodiment, analogous diagnostic and prognostic assays can be conducted with the marker protein or nucleotide and the probe as solutes in a liquid phase. In such an assay, complexes comprising the marker protein or nucleotide and the probe are separated from uncomplexed components by any of a number of standard techniques, including but not limited to: differential centrifugation, chromatography, electrophoresis and immunoprecipitation. In differential centrifugation, such complexes may be separated from uncomplexed assay components through a series of centrifugal steps, due to the different sedimentation equilibria of complexes based on their different sizes and densities (see, for example, Rivas, G., and Minton, A.P., 1993, *Trends Biochem Sci.* 18(8):284-7). Standard chromatographic techniques may also be utilized to separate such complexes from uncomplexed components. For example, gel filtration chromatography separates molecules based on size, and through the utilization of an appropriate gel filtration resin in a column format, for example, the relatively larger complexes may be separated from the relatively smaller uncomplexed components. Similarly, the different charge properties of such complexes as compared to the uncomplexed components may be exploited to differentiate the complexes from uncomplexed components, for example through the utilization of ion-exchange chromatography resins. Such resins and chromatographic techniques are well known to one skilled in the art (see, *e.g.*, Heegaard, N.H., 1998, *J. Mol. Recognit.* Winter 11(1-6): [__] **141-148**; Hage, D.S., and Tweed, S.A. *J Chromatogr B Biomed Sci Appl* 1997 Oct 10;699(1-2):499-525). Gel electrophoresis may also be employed to separate such complexes

from unbound components (see, *e.g.*, Ausubel *et al.*, ed., *Current Protocols in Molecular Biology*, John Wiley & Sons, New York, 1987-1999). In this technique, protein or nucleic acid complexes are separated based on size or charge, for example. In order to maintain the binding interaction during the electrophoretic process, non-denaturing gel matrix materials and conditions in the absence of reducing agent are typically preferred. Appropriate conditions to the particular assay and components thereof will be well known to one skilled in the art.